

10/567764

1 IAP5 Rec'd PCT/PTO 10 FEB 2006
SEQUENCE LISTING

<110> Wyeth
Flannery, Carl R
Corcoran, Christopher J
Freeman, Bethany A
Racie, Lisa A

<120> RECOMBINANT LUBRICIN MOLECULES AND USES THEREOF

<130> 50657-01404WOPT

<160> 29

<170> PatentIn version 3.3

<210> 1
<211> 155
<212> DNA
<213> Artificial

<220>

<223> Nucleotide sequence of synthetic cDNA cassette-1.

<400> 1
cgcgccca actccaaaag agcccgacc taccacgaca aagtcagctc ctactacgcc 60
caaagagcca gcgccgacga ctactaaaga accggcaccc accacgccta aggagccagc 120
tcctactaca acgaaaccgg caccaaccac tccgg 155

<210> 2
<211> 51
<212> PRT
<213> Artificial

<220>

<223> Translation of SEQ ID NO: 1.

<400> 2

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
1 5 10 15
Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
20 25 30
Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Pro Ala Pro
35 40 45
Thr Thr Pro
50

<210> 3
<211> 125
<212> DNA
<213> Artificial

<220>

<223> Nucleotide sequence of synthetic cDNA cassette-2.

<400> 3

```

taaagaacca gccöctacta cgacaaagga gcctgcaccc acaaccacga agagcgcacc      60
cacaacacca aaggagccgg cccctacgac tcctaaggaa cccaaaccgg caccaaccac      120
tccgg                                             125

```

<210> 4

<211> 41

<212> PRT

<213> Artificial

<220>

<223> Translation of SEQ ID NO: 3.

<400> 4

```

Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr Thr Thr
1          5          10          15
Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Pro Lys
          20          25          30
Glu Pro Lys Pro Ala Pro Thr Thr Pro
          35          40

```

<210> 5

<211> 8049

<212> DNA

<213> Artificial

<220>

<223> pTmed2 vector containing recombinant PRG4-Lub:1 cDNA construct.

<400> 5

```

catatgcggt gtgaaatacc gcacagatgc gtaaggagaa aataccgcat caggcgtact      60
gagtcattag ggactttcca atgggttttg ccagtagcat aaggtaata ggggtgaatc      120
aacaggaaag tcccattgga gccaaagtaca ctgagtcaat agggactttc cattgggttt      180
tgcccagtac aaaaggtcaa taggggggtga gtcaatgggt ttttccatt attggcacgt      240
acataagggtc aataggggtg agtcattggg tttttccagc caatttaatt aaaacgccat      300
gtactttccc accattgacg tcaatgggct attgaaacta atgcaacgtg acctttaaac      360
ggtagtttcc catagctgat taatgggaaa gtaccgttct cgagccaata caggtcaatg      420
ggaagtgaaa gggcagccaa aacgtaacac cgccccggtt tccccctgga aattccatat      480
tggcacgcat tctattggct gagctgcgtt ctacgtgggt ataagaggcg cgaccagcgt      540

```

cggtaccgtc gcagtcttcg gtctgaccac cgtagaacgc agagctcctc gctgcagccc	600
aagctctgtt gggctcgcgg ttgaggacaa actcttcgcg gtctttccag tactcttgga	660
tcggaaaccc gtcggcctcc gaacggtact ccgccaccga gggacctgag cgagtcgcga	720
tcgaccggat cggaaaacct ctcgactgtt ggggtgagta ctccctctca aaagcgggca	780
tgactttctgc gctaagattg tcagttttcca aaaacgagga ggatttgata ttcacctggc	840
ccgcggtgat gcctttgagg gtggccgcgt ccatctggtc agaaaagaca atctttttgt	900
tgtcaagctt gaggtgtggc aggcttgaga totggccata cacttgagtg acaatgacat	960
ccactttgcc tttctctcca caggtgtcca ctcccaggtc caactgcaga cttegaattc	1020
tactgagtcg acccaccatg gcatggaaaa cacttcccat ttacctgttg ttgctgctgt	1080
ctgttttcgt gattcagcaa gtttcatctc aagatttatc aagctgtgca gggagatgtg	1140
gggaagggtta ttctagagat gccacctgca actgtgatta taactgtcaa cactacatgg	1200
agtgtctccc tgatttcaag agagtctgca ctgcggagct ttctgtaaa ggccgctgct	1260
ttgagtcctt cgagagaggg agggagtgtg actgcgacgc ccaatgtaag aagtatgaca	1320
agtgtgtgcc cgattatgag agtttctgtg cagaagtgca taatcccaca tcaccaccat	1380
cttcaaagaa agcacctcca ctttcaggag catctcaaac catcaaatca acaaccaaac	1440
gttcacccaa accaccaaac aagaagaaga ctaagaaagt tatagaatca gaggaataa	1500
cagaagaaca ttctgtttct gaaaatcaag agtcctcctc cagtagcagt tcaagtagtt	1560
cgtcgtcgac aatttgaaa atcaagtctt caaaaattc agctgctaata agagaattac	1620
agaagaaact caaagtaaaa gataacaaga agaacagaac taaaaagaaa cctaccccca	1680
aaccaccagt ttagatgaa gctggaagtg gattggacaa tgggtgacttc aaggtcacaa	1740
ctcctgacac gtctaccacc caacacaata aagtcagcac atctcccaag atcacaacag	1800
caaaaccaat aaatccaga ccagtcctc cacctaattc tgatacatct aaagagacgt	1860
ctttgacagt gaataaagag acaacagttg aaactaaaga aactactaca acaaataaac	1920
agacttcaac tgatggaaaa gagaagacta cttccgctaa agagacacaa agtatagaga	1980
aaacatctgc taaagattta gcaccacat ctaaagtgtt ggctaaacct acacccaaag	2040
ctgaaactac aaccaaaggc cctgctctca ccactcccaa ggagcccacg cccaccactc	2100
ccaaggagcc tgcatctacc acacccaaag agcccacacc taccaccatc aagagcgcgc	2160
ccacaactcc aaaagagccc gcacctacca cgacaaagtc agctcctact acgcccacaaag	2220
agccagcgcc gacgactact aaagaaccgg caccacaccac gcctaaggag ccagctccta	2280
ctacaacgaa accggcacca accactccgg aaacacctcc tccaaccact tcagaggtct	2340

ctactccaac taccaccaag gagcctacca ctatccacaa aagccctgat gaatcaactc 2400
ctgagctttc tgcagaaccc acacccaaaag ctcttgaaaa cagtccccaag gaacctggtg 2460
tacctacaac taagacgccg gcggcgacta aacctgaaat gactacaaca gctaaagaca 2520
agacaacaga aagagactta cgtactacac ctgaaactac aactgctgca cctaagatga 2580
caaaagagac agcaactaca acagaaaaaa ctaccgaatc caaaataaca gctacaacca 2640
cacaagtaac atctaccaca actcaagata ccacaccatt caaaattact actcttaaaa 2700
caactactct tgcacccaaa gtaactacaa caaaaaagac aattactacc actgagatta 2760
tgaacaaacc tgaagaaaca gctaaaccaa aagacagagc tactaattct aaagcgacaa 2820
ctcctaaacc tcaaaagcca accaaagcac caaaaaacc cacttctacc aaaaagccaa 2880
aaacaatgcc tagagtgaga aaaccaaaga cgacaccaac tccccgcaag atgacatcaa 2940
caatgccaga attgaacct acctcaagaa tagcagaagc catgctccaa accaccacca 3000
gacctacca aactccaaac tccaaactag ttgaagtaaa tccaaagagt gaagatgcag 3060
gtggtgctga aggagaaaca cctcatatgc ttctcaggcc ccatgtgttc atgcctgaag 3120
ttactcccga catggattac ttaccgagag tacccaatca aggcattatc atcaatccca 3180
tgctttccga tgagaccaat atatgcaatg gtaagccagt agatggactg actactttgc 3240
gcaatgggac attagttgca ttccgaggtc attattttctg gatgctaagt ccattcagtc 3300
caccatctcc agctcgaga attactgaag tttggggtat tccttcccc attgatactg 3360
tttttactag gtgcaactgt gaaggaaaaa cttttotttt taaggattct cagtactggc 3420
gttttacc aa tgatataaaa gatgcagggt accccaaacc aattttcaaa ggatttggag 3480
gactaactgg acaaatagtg gcagcgcttt caacagctaa atataagaac tggcctgaat 3540
ctgtgtat tttcaagaga ggtggcagca ttcagcagta tatttataaa caggaacctg 3600
tacagaagt ccctggaaga aggcctgctc taaattatcc agtgtatgga gaaatgacac 3660
aggttaggag acgtcgcttt gaacgtgcta taggaccttc tcaaacacac accatcagaa 3720
ttcaatat acctgccaga ctggcttatc aagacaaagg tgtccttcat aatgaagtta 3780
aagtgagtat actgtggaga ggacttccaa atgtgggttac ctgagctata tcaactgccc 3840
acatcagaaa acctgacggc tatgattact atgccttttc taaagatcaa tactataaca 3900
ttgatgtgcc tagtagaaca gcaagagcaa ttactactcg ttctgggcag accttatcca 3960
aagtctggt caactgtcct taagcggccg ccgcaaattc taacgttact ggccgaagcc 4020
gcttgaata aggcgggtgt gcgtttgtct atatgttatt ttccaccata ttgccgtctt 4080

ttggcaatgt	gagggcccg	aaacctggcc	ctgtcttctt	gacgagcatt	cctaggggtc	4140
tttcccctct	cgccaaagga	atgcaaggtc	tgttgaatgt	cgtgaaggaa	gcagttcctc	4200
tggaagcttc	ttgaagacaa	acaacgtctg	tagcgaccct	ttgcaggcag	cggaaccccc	4260
cacctggcga	caggtgcctc	tgcggccaaa	agccacgtgt	ataagataca	cctgcaaagg	4320
cggcacaacc	ccagtgccac	gttgtgagtt	ggatagttgt	ggaaagagtc	aaatggctct	4380
cctcaagcgt	attcaacaag	gggctgaagg	atgccagaa	ggtaccccat	tgtatgggat	4440
ctgatctggg	gcctcgggtg	acatgcttta	catgtgttta	gtcgaggtta	aaaaacgtct	4500
agggcccccg	aaccacgggg	acgtggtttt	cctttgaaaa	acacgattgc	tcgagccatc	4560
atggttcgac	cattgaactg	catcgtcgcc	gtgtcccaaa	atatggggat	tggcaagaac	4620
ggagacctac	cctggcctcc	gctcaggaac	gagttcaagt	aottccaaag	aatgaccaca	4680
acctcttcag	tggaaggtaa	acagaatctg	gtgattatgg	gtaggaaaac	ctggttctcc	4740
attcctgaga	agaatcgacc	tttaaaggac	agaattaata	tagttctcag	tagagaactc	4800
aaagaaccac	cacgaggagc	tcatTTTTctt	gccaaaagtt	tggatgatgc	cttaagactt	4860
attgaacaac	cggaattggc	aagtaaagta	gacatggttt	ggatagtcgg	aggcagttct	4920
gtttaccagg	aagccatgaa	tcaaccaggc	cacctcagac	tctttgtgac	aaggatcatg	4980
caggaatttg	aaagtgacac	gtttttccca	gaaattgatt	tggggaaaata	taaacttctc	5040
ccagaatacc	caggcgctct	ctctgaggtc	caggaggaaa	aaggcatcaa	gtataagttt	5100
gaagtctacg	agaagaaaga	ctaacaggaa	gatgctttca	agttctctgc	tcccctccta	5160
aagctatgca	ttttttataa	gaccatggga	cttttgctgg	cttttagatca	taatcagcca	5220
taccacattt	gtagagggtt	tacttgcttt	aaaaaacctc	ccacacctcc	ccctgaacct	5280
gaaacataaa	atgaatgcaa	ttgttgttgt	taacttgttt	attgcagctt	ataatggtta	5340
caaataaagc	aatagcatca	caaatttcac	aaataaagca	tttttttcac	tgcattctag	5400
ttgtggtttg	tccaaactca	tcaatgtatc	ttatcatgtc	tggatccccg	gccaacggtc	5460
tggtgaccgg	gctgcgagag	ctcgggtgtac	ctgagacgcg	agtaagccct	tgagtcaaag	5520
acgtagtcgt	tgcaagtccg	caccagggtac	tgatcatoga	tgctagaccg	tgcaaaagga	5580
gagcctgtaa	gcgggcactc	ttccgtggtc	tggtggataa	attcgcaagg	gtatcatggc	5640
ggacgaccgg	ggttcgaacc	ccggatccgg	ccgtccgccc	tgatccatcc	ggttaccgcc	5700
cgcgtgtcga	accaggtgt	gcgacgtcag	acaacggggg	agcgtcctt	ttggcttctt	5760
tccaggcgcg	gcggtgctg	cgctagcttt	tttggcgagc	tcgaattaat	tctgcattaa	5820
tgaatcggcc	aacgcgcggg	gagaggcggt	ttgcgtattg	ggcgctcttc	cgttctctcg	5880

ctcactgact cgctgcgctc ggtcggttcgg ctgcggcgag cggtatcagc tcactcaaag 5940
gcggtataac ggttatccac agaatacagg gataacgcag gaaagaacat gtgagcaaaa 6000
ggccagcaaa aggccaggaa ccgtaaaaag gccgcgttgc tggcgttttt ccataggctc 6060
cgccccctg acgagcatca caaaaatcga cgctcaagtc agaggtggcg aaaccgcaca 6120
ggactataaa gataccaggc gtttccccct ggaagctccc tcgtgcgctc tcctgttccg 6180
accctgccgc ttaccggata cctgtccgce tttctccctt cgggaagcgt ggcgctttct 6240
caatgctcac gctgtaggta tctcagttcg gtgtaggtcg ttcgctccaa gctgggctgt 6300
gtgcacgaac cccccgttca gccgcaccgc tgcgccttat ccggttaacta tcgtcttgag 6360
tccaaccggg taagacacga cttatcgcca ctggcagcag ccactggtaa caggattagc 6420
agagcgaggt atgtaggcgg tgctacagag ttcttgaagt ggtggcctaa ctacggctac 6480
actagaagga cagtatttgg tatctgcgct ctgctgaagc cagttacctt cggaaaaaga 6540
gttggttagct cttgatccgg caaacaacc accgctggta gcggtggttt ttttgtttgc 6600
aagcagcaga ttacgcgcag aaaaaaagga tctcaagaag atcctttgat cttttctacg 6660
gggtctgacg ctcaagtggaa cgaaaactca cgtaaggga ttttggtcat gagattatca 6720
aaaaggatct tcacctagat ctttttaaat taaaaatgaa gttttaaatc aatctaaagt 6780
atatatgagt aaacttggtc tgacagttac caatgcttaa tcagtgggc acctatctca 6840
gcgatctgtc tatttcgttc atccatagtt gcctgactcc ccgtcgtgta gataactacg 6900
atacgggagg gcttaccatc tggccccagt gctgcaatga taccgcgaga cccacgctca 6960
ccggctccag atttatcagc aataaaccag ccagccggaa gggccgagcg cagaagtggg 7020
cctgcaactt tatccgcctc catccagtct attaattgtt gccgggaagc tagagtaagt 7080
agttcgccag ttaatagttt gcgcaacggt gttgccattg ctacaggcat cgtgggtgta 7140
cgctcgtcgt ttggtatggc ttcatcagc tccggttccc aacgatcaag gcgagttaca 7200
tgatccccca tgttgtgcaa aaaagcgggt agtccttcg gtcctccgat cgttgtcaga 7260
agtaagttgg ccgcagtgtt atcactcatg gttatggcag cactgcataa ttctcttact 7320
gtcatgccat ccgtaagatg cttttctgtg actgggtgagt actcaaccaa gtcattctga 7380
gaatagtgtg tgccggcgacc gagttgctct tgcccggcgt caatacggga taataccgcg 7440
ccacatagca gaactttaaa agtgctcatc attggaaaac gttcttcggg gcgaaaactc 7500
tcaaggatct taccgctgtt gagatccagt tcgatgtaac ccactcgtgc acccaactga 7560
tcttcagcat cttttacttt caccagcgtt tctgggtgag caaaaacagg aaggcaaat 7620

gccgcaaaaa aggggaataag ggcgacacgg aaatgttgaa tactcatact cttccttttt 7680
 caatattatt gaagcattta tcagggttat tgtctcatga gcggatacat atttgaatgt 7740
 atttagaaaa ataaacaaat aggggttccg cgcacatttc cccgaaaagt gccacctgac 7800
 gtctaagaaa ccattattat catgacatta acctataaaa ataggcgtat cacgaggccc 7860
 ttctgtctcg cgcgtttcgg tgatgacggg gaaaacctct gacacatgca gctcccgag 7920
 acggtcacag cttgtctgta agcggatgcc gggagcagac aagcccgta gggcgcgta 7980
 gcgggtgttg gcgggtgtcg gggctggctt aactatgcgg catcagagca gattgtactg 8040
 agagtgcac 8049

<210> 6
 <211> 2946
 <212> DNA
 <213> Artificial

<220>
 <223> Recombinant PRG4-Lub:1 cDNA construct.

<400> 6
 atggcatgga aaacacttcc catttacctg ttgttgctgc tgtctgtttt cgtgattcag 60
 caagtttcat ctcaagattt atcaagctgt gcaggagat gtggggaagg gtattctaga 120
 gatgccacct gcaactgtga ttataactgt caacactaca tggagtgtcg ccctgatttc 180
 aagagagtct gcaactgcga gctttcctgt aaaggccgt gctttgagtc cttcgagaga 240
 gggagggagt gtgactgca cgcccaatgt aagaagtatg acaagtgtcg tcccgattat 300
 gagagtttct gtgcagaagt gcataatccc acatcaccac catcttcaaa gaaagcacct 360
 ccaccttcag gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca 420
 aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt 480
 tctgaaaatc aagagtcctc ctccagtagc agttcaagta gttcgtcgtc gacaatttgg 540
 aaaatcaagt cttccaaaaa ttcagctgct aatagagaat tacagaagaa actcaaagta 600
 aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaacacc agttgtagat 660
 gaagctggaa gtggattgga caatggtgac ttcaaggta caactcctga cacgtctacc 720
 acccaacaca ataaagtcag cacatctccc aagatcaca cagcaaaacc aataaatccc 780
 agaccagtc ttccacctaa ttctgataca tctaaagaga cgtctttgac agtgaataaa 840
 gagacaacag ttgaaactaa agaaactact acaacaata aacagacttc aactgatgga 900
 aaagagaaga ctacttccgc taaagagaca caaagtatag agaaaacatc tgctaaagat 960
 ttagcaccca catctaaagt gctggctaaa cctacacca aagctgaaac tacaaccaa 1020

ggcctgctc	tcaccactcc	caaggagccc	acgcccacca	ctcccaagga	gcctgcatct	1080
accacaccca	aagagcccac	acctaccacc	atcaagagcg	cgcccacaac	tccaaaagag	1140
cccgaccta	ccacgacaaa	gtcagctcct	actacgccc	aagagccagc	gcgacgact	1200
actaaagaac	cggcaccac	cagcctaag	gagccagctc	ctactacaac	gaaaccggca	1260
ccaaccactc	cggaaacacc	tcctccaacc	acttcagagg	tctctactcc	aactaccacc	1320
aaggagccta	ccactatcca	caaaagccct	gatgaatcaa	ctcctgagct	ttctgcagaa	1380
cccacaccaa	aagctcttga	aaacagtccc	aaggaacctg	gtgtacctac	aactaagacg	1440
ccggcgggcg	ctaaacctga	aatgactaca	acagctaaag	acaagacaac	agaaagagac	1500
ttacgtacta	cacctgaaac	tacaactgct	gcacctaaag	tgacaaaaga	gacagcaact	1560
acaacagaaa	aaactaccga	atccaaaata	acagctacaa	ccacacaagt	aacatctacc	1620
acaactcaag	ataccacacc	attcaaaatt	actactctta	aaacaactac	tcttgcaccc	1680
aaagtaacta	caacaaaaaa	gacaattact	accactgaga	ttatgaacaa	acctgaagaa	1740
acagctaaac	caaaagacag	agctactaat	tctaaagcga	caactcctaa	acctcaaaag	1800
ccaaccaaa	cacccaaaaa	accacttct	acccaaaagc	caaaaacaat	gcctagagtg	1860
agaaaaccaa	agacgacacc	aactccccgc	aagatgacat	caacaatgcc	agaattgaac	1920
cctacctcaa	gaatagcaga	agccatgctc	caaaccacca	ccagacctaa	cctaaactcca	1980
aactccaaac	tagttgaagt	aatccaaag	agtgaagatg	caggtggtgc	tgaaggagaa	2040
acacctcata	tgcttctcag	gccccatgtg	ttcatgcctg	aagttactcc	cgacatggat	2100
tacttaccga	gagtacccaa	tcaaggcatt	atcatcaatc	ccatgctttc	cgatgagacc	2160
aatatatgca	atggtaagcc	agtagatgga	ctgactactt	tgcgcaatgg	gacattagtt	2220
gcattccgag	gtcattatct	ctggatgcta	agtcatttca	gtccaccatc	tccagctcgc	2280
agaattactg	aagtttgggg	tattccttcc	cccattgata	ctgtttttac	taggtgcaac	2340
tgtgaaggaa	aaactttctt	ctttaaggat	tctcagtact	ggcgttttac	caatgatata	2400
aaagatgcag	ggtaccccaa	accaattttc	aaaggatttg	gaggactaac	tggacaaata	2460
gtggcagcgc	tttcaacagc	taaatataag	aactggcctg	aatctgtgta	ttttttcaag	2520
agaggtggca	gcattcagca	gtatatattat	aaacaggaac	ctgtacagaa	gtgccctgga	2580
agaaggcctg	ctctaaatta	tccagtgtat	ggagaaatga	cacaggttag	gagacgtcgc	2640
tttgaacgtg	ctataggacc	ttctcaaaca	cacaccatca	gaattcaata	ttcacctgcc	2700
agactggctt	atcaagacaa	aggtgtcctt	cataatgaag	ttaaagttag	tatactgtgg	2760

agaggacttc caaatgtggt tacctcagct atatcactgc ccaacatcag aaaacctgac 2820
 ggctatgatt actatgcctt ttctaaagat caatactata acattgatgt gcctagtaga 2880
 acagcaagag caattactac tcgttctgga cagaccttat ccaaagtctg gtacaactgt 2940
 ccttaa 2946

<210> 7
 <211> 981
 <212> PRT
 <213> Artificial

<220>

<223> Amino acid sequence of entire PRG4-LUB:1 protein.

<400> 7

Met Ala Trp Lys Thr Leu Pro Ile Tyr Leu Leu Leu Leu Leu Ser Val
 1 5 10 15
 Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly
 20 25 30
 Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr
 35 40 45
 Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys
 50 55 60
 Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg
 65 70 75 80
 Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys
 85 90 95
 Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser
 100 105 110
 Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr
 115 120 125
 Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys
 130 135 140
 Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val
 145 150 155 160
 Ser Glu Asn Gln Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
 165 170 175
 Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg
 180 185 190
 Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr
 195 200 205
 Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser

210				215				220							
Gly 225	Leu	Asp	Asn	Gly 230	Asp	Phe	Lys	Val	Thr 235	Thr 235	Pro	Asp	Thr	Ser	Thr 240
Thr	Gln	His	Asn	Lys 245	Val	Ser	Thr	Ser	Pro 250	Lys	Ile	Thr	Thr	Ala	Lys 255
Pro	Ile	Asn	Pro	Arg 260	Pro	Ser	Leu	Pro	Pro 265	Asn	Ser	Asp	Thr	Ser	Lys 270
Glu	Thr	Ser	Leu	Thr 275	Val	Asn	Lys 280	Glu	Thr	Thr	Val	Glu 285	Thr	Lys	Glu
Thr	Thr	Thr	Thr	Asn	Lys	Gln 295	Thr	Ser	Thr	Asp	Gly 300	Lys	Glu	Lys	Thr
Thr 305	Ser	Ala	Lys	Glu	Thr	Gln 310	Ser	Ile	Glu	Lys 315	Thr	Ser	Ala	Lys	Asp 320
Leu	Ala	Pro	Thr	Ser 325	Lys	Val	Leu	Ala	Lys 330	Pro	Thr	Pro	Lys	Ala	Glu 335
Thr	Thr	Thr	Lys 340	Gly	Pro	Ala	Leu	Thr	Thr 345	Pro	Lys	Glu	Pro	Thr	Pro 350
Thr	Thr	Pro	Lys 355	Glu	Pro	Ala	Ser	Thr	Thr 360	Pro	Lys	Glu	Pro	Thr	Pro 365
Thr	Thr	Ile	Lys	Ser	Ala	Pro 375	Thr	Thr	Pro	Lys	Glu 380	Pro	Ala	Pro	Thr 385
Thr 385	Thr	Lys	Ser	Ala	Pro 390	Thr	Thr	Pro	Lys	Glu 395	Pro	Ala	Pro	Thr	Thr 400
Thr	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Pro	Lys 410	Glu	Pro	Ala	Pro	Thr	Thr 415
Thr	Lys	Pro	Ala	Pro	Thr	Thr	Pro	Glu	Thr 425	Pro	Pro	Pro	Thr	Thr	Ser 430
Glu	Val	Ser	Thr	Pro	Thr	Thr	Thr	Lys	Glu	Pro	Thr	Thr	Ile	His	Lys 445
Ser	Pro	Asp	Glu	Ser	Thr	Pro	Glu	Leu	Ser	Ala	Glu 460	Pro	Thr	Pro	Lys 450
Ala	Leu	Glu	Asn	Ser	Pro	Lys	Glu	Pro	Gly	Val	Pro	Thr	Thr	Lys	Thr 480
Pro	Ala	Ala	Thr	Lys 485	Pro	Glu	Met	Thr	Thr	Thr	Ala	Lys	Asp	Lys	Thr 495
Thr	Glu	Arg	Asp	Leu	Arg	Thr	Thr	Pro	Glu	Thr	Thr	Thr	Ala	Ala	Pro 510
Lys	Met	Thr	Lys	Glu	Thr	Ala	Thr	Thr	Thr	Glu	Lys	Thr	Thr	Glu	Ser 525

Lys Ile Thr Ala Thr Thr Thr Gln Val Thr Ser Thr Thr Thr Gln Asp
 530 535 540
 Thr Thr Pro Phe Lys Ile Thr Thr Leu Lys Thr Thr Thr Leu Ala Pro
 545 550 555 560
 Lys Val Thr Thr Thr Lys Lys Thr Ile Thr Thr Thr Glu Ile Met Asn
 565 570 575
 Lys Pro Glu Glu Thr Ala Lys Pro Lys Asp Arg Ala Thr Asn Ser Lys
 580 585 590
 Ala Thr Thr Pro Lys Pro Gln Lys Pro Thr Lys Ala Pro Lys Lys Pro
 595 600 605
 Thr Ser Thr Lys Lys Pro Lys Thr Met Pro Arg Val Arg Lys Pro Lys
 610 615 620
 Thr Thr Pro Thr Pro Arg Lys Met Thr Ser Thr Met Pro Glu Leu Asn
 625 630 635 640
 Pro Thr Ser Arg Ile Ala Glu Ala Met Leu Gln Thr Thr Thr Arg Pro
 645 650 655
 Asn Gln Thr Pro Asn Ser Lys Leu Val Glu Val Asn Pro Lys Ser Glu
 660 665 670
 Asp Ala Gly Gly Ala Glu Gly Glu Thr Pro His Met Leu Leu Arg Pro
 675 680 685
 His Val Phe Met Pro Glu Val Thr Pro Asp Met Asp Tyr Leu Pro Arg
 690 695 700
 Val Pro Asn Gln Gly Ile Ile Ile Asn Pro Met Leu Ser Asp Glu Thr
 705 710 715 720
 Asn Ile Cys Asn Gly Lys Pro Val Asp Gly Leu Thr Thr Leu Arg Asn
 725 730 735
 Gly Thr Leu Val Ala Phe Arg Gly His Tyr Phe Trp Met Leu Ser Pro
 740 745 750
 Phe Ser Pro Pro Ser Pro Ala Arg Arg Ile Thr Glu Val Trp Gly Ile
 755 760 765
 Pro Ser Pro Ile Asp Thr Val Phe Thr Arg Cys Asn Cys Glu Gly Lys
 770 775 780
 Thr Phe Phe Phe Lys Asp Ser Gln Tyr Trp Arg Phe Thr Asn Asp Ile
 785 790 795 800
 Lys Asp Ala Gly Tyr Pro Lys Pro Ile Phe Lys Gly Phe Gly Gly Leu
 805 810 815
 Thr Gly Gln Ile Val Ala Ala Leu Ser Thr Ala Lys Tyr Lys Asn Trp
 820 825 830
 Pro Glu Ser Val Tyr Phe Phe Lys Arg Gly Gly Ser Ile Gln Gln Tyr
 835 840 845

Ile Tyr Lys Gln Glu Pro Val Gln Lys Cys Pro Gly Arg Arg Pro Ala
 850 855 860
 Leu Asn Tyr Pro Val Tyr Gly Glu Met Thr Gln Val Arg Arg Arg Arg
 865 870 875 880
 Phe Glu Arg Ala Ile Gly Pro Ser Gln Thr His Thr Ile Arg Ile Gln
 885 890 895
 Tyr Ser Pro Ala Arg Leu Ala Tyr Gln Asp Lys Gly Val Leu His Asn
 900 905 910
 Glu Val Lys Val Ser Ile Leu Trp Arg Gly Leu Pro Asn Val Val Thr
 915 920 925
 Ser Ala Ile Ser Leu Pro Asn Ile Arg Lys Pro Asp Gly Tyr Asp Tyr
 930 935 940
 Tyr Ala Phe Ser Lys Asp Gln Tyr Tyr Asn Ile Asp Val Pro Ser Arg
 945 950 955 960
 Thr Ala Arg Ala Ile Thr Thr Arg Ser Gly Gln Thr Leu Ser Lys Val
 965 970 975
 Trp Tyr Asn Cys Pro
 980

<210> 8
 <211> 157
 <212> DNA
 <213> Artificial

<220>
 <223> Lub:1 DNA insert from synthetic cDNA cassette-1.

<400> 8
 gcgcgcccac aactccaaaa gagcccgac ctaccacgac aaagtcagct cctactacgc 60
 ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaggagccag 120
 ctctactac aacgaaaccg gcaccaacca ctccgga 157

<210> 9
 <211> 51
 <212> PRT
 <213> Artificial

<220>
 <223> 51 amino acids encoded by Lub:1 DNA insert (4 KEPAPTT sequences between S373 to E425 in SEQ ID NO: 7).

<400> 9

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
 1 5 10 15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
 20 25 30
 Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Pro Ala Pro
 35 40 45
 Thr Thr Pro
 50

<210> 10
 <211> 3024
 <212> DNA
 <213> Artificial

<220>
 <223> Recombinant PRG4-Lub:2 cDNA construct.

<400> 10
 atggcatgga aaacacttcc catttacctg ttgttgctgc tgtctgtttt cgtgattcag 60
 caagtttcat ctcaagattt atcaagctgt gcagggagat gtggggaagg gtattctaga 120
 gatgccacct gcaactgtga ttataactgt caacactaca tggagtgtctg ccctgatttc 180
 aagagagtct gcaactgcgga gctttcctgt aaaggccgct gctttgagtc cttcgagaga 240
 gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgtctg tcccgattat 300
 gagagtttct gtgcagaagt gcataatccc acatcaccac catcttcaaa gaaagcacct 360
 ccaccttcag gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca 420
 aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt 480
 tctgaaaatc aagagtcctc ctccagtagc agttcaagta gttcgtcgtc gacaatttgg 540
 aaaatcaagt cttccaaaaa ttcagctgct aatagagaat tacagaagaa actcaaagta 600
 aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgtagat 660
 gaagctggaa gtggattgga caatggtgac ttcaaggta caactcctga cagctctacc 720
 acccaacaca ataaagtcag cacatctccc aagatcacaa cagcaaaacc aataaatccc 780
 agaccagtc ttccacctaa ttctgatata tctaaagaga cgtctttgac agtgaataaa 840
 gagacaacag ttgaaactaa agaaactact acaacaata aacagacttc aactgatgga 900
 aaagagaaga ctacttccgc taaagagaca caaagtatag agaaaacatc tgctaaagat 960
 ttagcaccca catctaaagt gctggctaaa cctacacca aagctgaaac tacaaccaa 1020
 ggccctgtc tcaccactcc caaggagccc acgccacca ctccaagga gcctgcatct 1080
 accacacca aagagcccac acctaccacc atcaagagcg cgcccacaac tccaaaagag 1140
 cccgcaccta ccacgacaaa gtcagctcct actacgcca aagagccagc gccgacgact 1200

actaaagaac cggcaccac cagcctaataa gaaccagccc ctactacgac aaaggagcct 1260
gcaccacaa ccacgaagag cgcaccaca acaccaaagg agccggcccc tacgactcct 1320
aaggaacca aaccggcacc aaccactccg gaaacacctc ctccaaccac ttcagaggtc 1380
tctactcaa ctaccacaa ggagcctacc actatccaca aaagccctga tgaatcaact 1440
cctgagcttt ctgcagaacc cacacaaaaa gctcttgaaa acagtcccaa ggaacctggt 1500
gtacctaca ctaagacgcc ggcggcgact aaacctgaaa tgactacaac agctaaagac 1560
aagacaacag aaagagactt acgtactaca cctgaaacta caactgctgc acctaatgatg 1620
acaaaagaga cagcaactac aacagaaaaa actaccgaat ccaaaataac agctacaacc 1680
acacaagtaa catctaccac aactcaagat accacaccat tcaaaattac tactcttaaa 1740
acaactactc ttgcaccaa agtaactaca acaaaaaaga caattactac cactgagatt 1800
atgaacaaac ctgaagaaac agctaaacca aaagacagag ctactaattc taaagcgaca 1860
actcctaaac ctcaaaagcc aaccaaagca ccaaaaaaac ccacttctac caaaaagcca 1920
aaaacaatgc ctagagtgcg aaaaccaaag acgacaccaa ctccccgcaa gatgacatca 1980
acaatgccag aattgaaccc tacctcaaga atagcagaag ccatgctcca aaccaccacc 2040
agacctaac aaactccaaa ctccaaacta gttgaagtaa atccaaagag tgaagatgca 2100
ggtggtgctg aaggagaaac acctcatatg cttctcaggc cccatgtgtt catgcctgaa 2160
gttactcccg acatggatta cttaccgaga gtacccaatc aaggcattat catcaatccc 2220
atgctttccg atgagaccaa tatatgcaat ggtaagccag tagatggact gactactttg 2280
cgcaatggga cattagtgc attccgaggt cattatttct ggatgctaag tccattcagt 2340
ccaccatctc cagctcgag aattactgaa gtttggggta ttccctcccc cattgatact 2400
gtttttacta ggtgcaactg tgaaggaaaa actttcttct ttaaggattc tcagtactgg 2460
cgtttttacca atgatataaa agatgcaggg taccctaaac caattttcaa aggatttgga 2520
ggactaactg gacaaatagt ggcagcgctt tcaacagcta aatataagaa ctggcctgaa 2580
tctgtgtatt ttttcaagag aggtggcagc attcagcagt atatttataa acaggaacct 2640
gtacagaagt gccctggaag aaggcctgct ctaaattatc cagtgtatgg agaaatgaca 2700
caggttagga gacgtcgctt tgaacgtgct ataggacctt ctcaaacaca caccatcaga 2760
attcaatatt cacctgccag actggcttat caagacaaag gtgtccttca taatgaagtt 2820
aaagtgaata tactgtggag aggacttcca aatgtggtta cctcagctat atcactgccc 2880
aacatcagaa aacctgacgg ctatgattac tatgcctttt ctaaagatca atactataac 2940
attgatgtgc ctagtagaac agcaagagca attactactc gttctgggca gaccttatcc 3000

aaagtctggt acaactgtcc ttaa

3024

<210> 11

<211> 1007

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of entire PRG4-LUB:2 protein.

<400> 11

Met Ala Trp Lys Thr Leu Pro Ile Tyr Leu Leu Leu Leu Leu Ser Val
 1 5 10 15

Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly
 20 25 30

Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr
 35 40 45

Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys
 50 55 60

Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg
 65 70 75 80

Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys
 85 90 95

Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser
 100 105 110

Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr
 115 120 125

Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys
 130 135 140

Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val
 145 150 155 160

Ser Glu Asn Gln Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
 165 170 175

Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg
 180 185 190

Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr
 195 200 205

Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser
 210 215 220

Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr
 225 230 235 240

Thr	Gln	His	Asn	Lys	Val	Ser	Thr	Ser	Pro	Lys	Ile	Thr	Thr	Ala	Lys	
				245					250					255		
Pro	Ile	Asn	Pro	Arg	Pro	Ser	Leu	Pro	Pro	Asn	Ser	Asp	Thr	Ser	Lys	
			260					265					270			
Glu	Thr	Ser	Leu	Thr	Val	Asn	Lys	Glu	Thr	Thr	Val	Glu	Thr	Lys	Glu	
		275					280					285				
Thr	Thr	Thr	Thr	Asn	Lys	Gln	Thr	Ser	Thr	Asp	Gly	Lys	Glu	Lys	Thr	
	290					295					300					
Thr	Ser	Ala	Lys	Glu	Thr	Gln	Ser	Ile	Glu	Lys	Thr	Ser	Ala	Lys	Asp	
305						310				315					320	
Leu	Ala	Pro	Thr	Ser	Lys	Val	Leu	Ala	Lys	Pro	Thr	Pro	Lys	Ala	Glu	
				325					330					335		
Thr	Thr	Thr	Lys	Gly	Pro	Ala	Leu	Thr	Thr	Pro	Lys	Glu	Pro	Thr	Pro	
			340					345					350			
Thr	Thr	Pro	Lys	Glu	Pro	Ala	Ser	Thr	Thr	Pro	Lys	Glu	Pro	Thr	Pro	
		355					360					365				
Thr	Thr	Ile	Lys	Ser	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	
	370					375					380					
Thr	Thr	Lys	Ser	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	
385					390					395					400	
Thr	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	
				405					410					415		
Thr	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	Ser	Ala	Pro	Thr	Thr	Pro	
			420					425					430			
Lys	Glu	Pro	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Lys	Pro	Ala	Pro	Thr	
		435					440					445				
Thr	Pro	Glu	Thr	Pro	Pro	Pro	Thr	Thr	Ser	Glu	Val	Ser	Thr	Pro	Thr	
	450					455					460					
Thr	Thr	Lys	Glu	Pro	Thr	Thr	Ile	His	Lys	Ser	Pro	Asp	Glu	Ser	Thr	
465					470					475				480		
Pro	Glu	Leu	Ser	Ala	Glu	Pro	Thr	Pro	Lys	Ala	Leu	Glu	Asn	Ser	Pro	
				485					490					495		
Lys	Glu	Pro	Gly	Val	Pro	Thr	Thr	Lys	Thr	Pro	Ala	Ala	Thr	Lys	Pro	
			500					505					510			
Glu	Met	Thr	Thr	Thr	Ala	Lys	Asp	Lys	Thr	Thr	Glu	Arg	Asp	Leu	Arg	
		515					520					525				
Thr	Thr	Pro	Glu	Thr	Thr	Thr	Ala	Ala	Pro	Lys	Met	Thr	Lys	Glu	Thr	
	530					535					540					
Ala	Thr	Thr	Thr	Glu	Lys	Thr	Thr	Glu	Ser	Lys	Ile	Thr	Ala	Thr	Thr	
545					550					555					560	

Thr Gln Val Thr Ser Thr Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile
 565 570 575
 Thr Thr Leu Lys Thr Thr Thr Leu Ala Pro Lys Val Thr Thr Thr Lys
 580 585 590
 Lys Thr Ile Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala
 595 600 605
 Lys Pro Lys Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro
 610 615 620
 Gln Lys Pro Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro
 625 630 635 640
 Lys Thr Met Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg
 645 650 655
 Lys Met Thr Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala
 660 665 670
 Glu Ala Met Leu Gln Thr Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser
 675 680 685
 Lys Leu Val Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu
 690 695 700
 Gly Glu Thr Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu
 705 710 715 720
 Val Thr Pro Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile
 725 730 735
 Ile Ile Asn Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys
 740 745 750
 Pro Val Asp Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe
 755 760 765
 Arg Gly His Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro
 770 775 780
 Ala Arg Arg Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr
 785 790 795 800
 Val Phe Thr Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp
 805 810 815
 Ser Gln Tyr Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro
 820 825 830
 Lys Pro Ile Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala
 835 840 845
 Ala Leu Ser Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe
 850 855 860
 Phe Lys Arg Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro

18

865		870		875		880
Val Gln Lys Cys Pro Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr						
		885		890		895
Gly Glu Met Thr Gln Val Arg Arg Arg Arg Phe Glu Arg Ala Ile Gly						
		900		905		910
Pro Ser Gln Thr His Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu						
		915		920		925
Ala Tyr Gln Asp Lys Gly Val Leu His Asn Glu Val Lys Val Ser Ile						
		930		935		940
Leu Trp Arg Gly Leu Pro Asn Val Val Thr Ser Ala Ile Ser Leu Pro						
		945		950		955
Asn Ile Arg Lys Pro Asp Gly Tyr Asp Tyr Tyr Ala Phe Ser Lys Asp						
		965		970		975
Gln Tyr Tyr Asn Ile Asp Val Pro Ser Arg Thr Ala Arg Ala Ile Thr						
		980		985		990
Thr Arg Ser Gly Gln Thr Leu Ser Lys Val Trp Tyr Asn Cys Pro						
		995		1000		1005

<210> 12
 <211> 235
 <212> DNA
 <213> Artificial

<220>

<223> Lub:2 DNA insert from synthetic cDNA cassette-1 and one synthetic cDNA cassette-2 sequence.

<400> 12	
gcgcgcccac aactccaaaa gagccgcac ctaccacgac aaagtcagct cctactacgc	60
ccaaagagcc agcgcgcgacg actactaaag aaccggcacc caccacgcct aaagaaccag	120
cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc acaacaccaa	180
aggagccggc ccctacgact cctaaggaac ccaaaccggc accaaccact ccgga	235

<210> 13
 <211> 77
 <212> PRT
 <213> Artificial

<220>

<223> 77 amino acids encoded by Lub:2 DNA insert (6 KEPAPTT sequences between S373 and E451 in SEQ ID NO: 11).

<400> 13

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
1 5 10 15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
 20 25 30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
 35 40 45

Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro
 50 55 60

Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
 65 70 75

<210> 14
 <211> 3117
 <212> DNA
 <213> Artificial

<220>
 <223> Recombinant PRG4-Lub:3 cDNA construct.

<400> 14
 atggcatgga aaacacttcc catttacctg ttgttgctgc tgtctgtttt cgtgattcag 60
 caagtttcat ctcaagattt atcaagctgt gcagggagat gtggggaagg gtattctaga 120
 gatgccacct gcaactgtga ttataactgt caaactaca tggagtgtctg ccttgatttc 180
 aagagagtct gcaactgcgga gctttcctgt aaaggccgct gctttgagtc cttcgagaga 240
 gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgtctg tcccgattat 300
 gagagtttct gtgcagaagt gcataatccc acatcaccac catcttcaaa gaaagcacct 360
 ccaccttcag gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca 420
 aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt 480
 tctgaaaatc aagagtcctc ctccagtagc agttcaagta gttcgtcgtc gacaatttgg 540
 aaaatcaagt cttccaaaaa ttcagctgct aatagagaat tacagaagaa actcaaagta 600
 aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgtagat 660
 gaagctggaa gtggattgga caatggtgac ttcaaggtca caactcctga cacgtctacc 720
 acccaacaca ataaagtcag cacatctccc aagatcacia cagcaaaacc aataaatccc 780
 agaccagtc ttccacctaa ttctgataca tctaaagaga cgtctttgac agtgaataaa 840
 gagacaacag ttgaaactaa agaaactact acaacaaata aacagacttc aactgatgga 900
 aaagagaaga ctacttccgc taaagagaca caaagtatag agaaaacatc tgctaaagat 960
 ttagcaccca catctaaagt gctggctaaa cctacacca aagctgaaac tacaaccaa 1020
 ggccctgctc tcaccactcc caaggagccc acgcccacca ctcccaagga gcctgcatct 1080

accacaccca aagagcccac acctaccacc atcaagagcg cgcccacaac tccaaaagag	1140
cccgcaccta ccacgacaaa gtcagctcct actacgcca aagagccagc gccgacgact	1200
actaaagaac cggcaccac cagcctaata gaaccagccc ctactacgac aaaggagcct	1260
gcaccacaaa ccacgaagag cgcaccacac acaccaaagg agccggcccc tacgactcct	1320
aaagaaccag cccctactac gacaaaggag cctgcacca caaccacgaa gagcgcaccc	1380
acaacaccaa aggagccggc ccctacgact cctaaggaac ccaaaccggc accaaccact	1440
ccggaacac ctctccaac cacttcagag gtctctactc caactaccac caaggagcct	1500
accactatcc acaaaagccc tgatgaatca actcctgagc tttctgcaga acccacacca	1560
aaagctcttg aaacagtc caaggaacct ggtgtaccta caactaagac gccggcgggc	1620
actaaacctg aaatgactac aacagctaaa gacaagacaa cagaaagaga cttacgtact	1680
acacctgaaa ctacaactgc tgcacctaa atgacaaaag agacagcaac tacaacagaa	1740
aaaactaccg aatccaaaat aacagctaca accacacaag taacatctac cacaactcaa	1800
gataccacac cattcaaaat tactactott aaacaacta ctcttgacc caaagtaact	1860
acaacaaaaa agacaattac taccactgag attatgaaca aacctgaaga aacagctaaa	1920
ccaaaagaca gagctactaa ttctaaagcg acaactccta aacctcaaaa gccaaccaaa	1980
gcacccaaaa aaccacttc taccaaaaag ccaaaaacaa tgcctagagt gagaaaacca	2040
aagacgacac caactccccg caagatgaca tcaacaatgc cagaattgaa ccctacctca	2100
agaatagcag aagccatgct ccaaaccacc accagaccta accaaactcc aaactccaaa	2160
ctagttgaag taaatccaaa gagtgaagat gcaggtgggt ctgaaggaga aacacctcat	2220
atgcttctca ggccccatgt gttcatgcct gaagtactc ccgacatgga ttacttaccg	2280
agagtacca atcaaggcat tatcatcaat cccatgcttt ccgatgagac caatatatgc	2340
aatggtaagc cagtagatgg actgactact ttgcgcaatg ggacattagt tgcattccga	2400
ggtcattatt tctggatgct aagtccattc agtccaccat ctccagctcg cagaattact	2460
gaagtttggg gtattccttc cccattgat actgttttta ctaggtgcaa ctgtgaagga	2520
aaaactttct tctttaagga ttctcagtac tggcgtttta ccaatgatat aaaagatgca	2580
gggtacccca aaccaatttt caaaggattt ggaggactaa ctggacaaat agtggcagcg	2640
ctttcaacag ctaaataata gaactggcct gaatctgtgt attttttcaa gagaggtggc	2700
agcattcagc agtatattta taaacaggaa cctgtacaga agtgccctgg aagaaggcct	2760
gctctaaatt atccagtgt tggagaaatg acacaggtta ggagacgtcg ctttgaacgt	2820
gctataggac cttctcaaac acacaccatc agaattcaat attcacctgc cagactggct	2880

tatcaagaca aaggtgtcct tcataatgaa gttaaagtga gtatactgtg gagaggactt 2940
 ccaaagtgtg ttacctcagc tatatcactg cccaacatca gaaaacctga cggctatgat 3000
 tactatgcct tttctaaaga tcaatactat aacattgatg tgcttagtag aacagcaaga 3060
 gcaattacta ctcgttctgg gcagacctta tccaaagtct ggtacaactg tccttaa 3117

<210> 15

<211> 1038

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of entire PRG4-LUB:3 protein

<400> 15

Met	Ala	Trp	Lys	Thr	Leu	Pro	Ile	Tyr	Leu	Leu	Leu	Leu	Leu	Ser	Val	1	5	10	15
Phe	Val	Ile	Gln	Gln	Val	Ser	Ser	Gln	Asp	Leu	Ser	Ser	Cys	Ala	Gly	20	25	30	
Arg	Cys	Gly	Glu	Gly	Tyr	Ser	Arg	Asp	Ala	Thr	Cys	Asn	Cys	Asp	Tyr	35	40	45	
Asn	Cys	Gln	His	Tyr	Met	Glu	Cys	Cys	Pro	Asp	Phe	Lys	Arg	Val	Cys	50	55	60	
Thr	Ala	Glu	Leu	Ser	Cys	Lys	Gly	Arg	Cys	Phe	Glu	Ser	Phe	Glu	Arg	65	70	75	80
Gly	Arg	Glu	Cys	Asp	Cys	Asp	Ala	Gln	Cys	Lys	Lys	Tyr	Asp	Lys	Cys	85	90	95	
Cys	Pro	Asp	Tyr	Glu	Ser	Phe	Cys	Ala	Glu	Val	His	Asn	Pro	Thr	Ser	100	105	110	
Pro	Pro	Ser	Ser	Lys	Lys	Ala	Pro	Pro	Pro	Ser	Gly	Ala	Ser	Gln	Thr	115	120	125	
Ile	Lys	Ser	Thr	Thr	Lys	Arg	Ser	Pro	Lys	Pro	Pro	Asn	Lys	Lys	Lys	130	135	140	
Thr	Lys	Lys	Val	Ile	Glu	Ser	Glu	Glu	Ile	Thr	Glu	Glu	His	Ser	Val	145	150	155	160
Ser	Glu	Asn	Gln	Glu	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	165	170	175	
Ser	Thr	Ile	Trp	Lys	Ile	Lys	Ser	Ser	Lys	Asn	Ser	Ala	Ala	Asn	Arg	180	185	190	
Glu	Leu	Gln	Lys	Lys	Leu	Lys	Val	Lys	Asp	Asn	Lys	Lys	Asn	Arg	Thr	195	200	205	

Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser
 210 215 220
 Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr
 225 230 235 240
 Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys
 245 250 255
 Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys
 260 265 270
 Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu
 275 280 285
 Thr Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr
 290 295 300
 Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp
 305 310 315 320
 Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu
 325 330 335
 Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro
 340 345 350
 Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro
 355 360 365
 Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
 370 375 380
 Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
 385 390 395 400
 Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
 405 410 415
 Thr Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro
 420 425 430
 Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr
 435 440 445
 Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys
 450 455 460
 Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr
 465 470 475 480
 Pro Glu Thr Pro Pro Pro Thr Thr Ser Glu Val Ser Thr Pro Thr Thr
 485 490 495
 Thr Lys Glu Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr Pro
 500 505 510
 Glu Leu Ser Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro Lys
 515 520 525

Glu Pro Gly Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro Glu
 530 535 540
 Met Thr Thr Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg Thr
 545 550 555 560
 Thr Pro Glu Thr Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr Ala
 565 570 575
 Thr Thr Thr Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr Thr
 580 585 590
 Gln Val Thr Ser Thr Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile Thr
 595 600 605
 Thr Leu Lys Thr Thr Thr Leu Ala Pro Lys Val Thr Thr Thr Lys Lys
 610 615 620
 Thr Ile Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala Lys
 625 630 635 640
 Pro Lys Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro Gln
 645 650 655
 Lys Pro Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro Lys
 660 665 670
 Thr Met Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg Lys
 675 680 685
 Met Thr Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala Glu
 690 695 700
 Ala Met Leu Gln Thr Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser Lys
 705 710 715 720
 Leu Val Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu Gly
 725 730 735
 Glu Thr Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu Val
 740 745 750
 Thr Pro Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile Ile
 755 760 765
 Ile Asn Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro
 770 775 780
 Val Asp Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe Arg
 785 790 795 800
 Gly His Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro Ala
 805 810 815
 Arg Arg Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr Val
 820 825 830
 Phe Thr Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp Ser

835	840	845
Gln Tyr Trp Arg Phe Thr	Asn Asp Ile Lys Asp	Ala Gly Tyr Pro Lys
850	855	860
Pro Ile Phe Lys Gly Phe	Gly Gly Leu Thr	Gly Gln Ile Val Ala Ala
865	870	875 880
Leu Ser Thr Ala Lys Tyr	Lys Asn Trp Pro Glu Ser	Val Tyr Phe Phe
885	890	895
Lys Arg Gly Gly Ser Ile	Gln Gln Tyr Ile Tyr	Lys Gln Glu Pro Val
900	905	910
Gln Lys Cys Pro Gly Arg	Arg Pro Ala Leu Asn Tyr	Pro Val Tyr Gly
915	920	925
Glu Met Thr Gln Val Arg	Arg Arg Arg Phe Glu Arg	Ala Ile Gly Pro
930	935	940
Ser Gln Thr His Thr Ile	Arg Ile Gln Tyr Ser Pro	Ala Arg Leu Ala
945	950	955 960
Tyr Gln Asp Lys Gly Val	Leu His Asn Glu Val	Lys Val Ser Ile Leu
965	970	975
Trp Arg Gly Leu Pro Asn	Val Val Thr Ser Ala Ile	Ser Leu Pro Asn
980	985	990
Ile Arg Lys Pro Asp Gly	Tyr Asp Tyr Tyr Ala Phe	Ser Lys Asp Gln
995	1000	1005
Tyr Tyr Asn Ile Asp Val	Pro Ser Arg Thr Ala Arg	Ala Ile Thr
1010	1015	1020
Thr Arg Ser Gly Gln Thr	Leu Ser Lys Val Trp Tyr	Asn Cys Pro
1025	1030	1035

<210> 16

<211> 328

<212> DNA

<213> Artificial

<220>

<223> Lub:3 DNA insert from synthetic cDNA cassette-1 and two synthetic cDNA cassette-2 sequences.

<400> 16

gcgcgccac aactcctaaa gagcccgac ctaccacgac aaagtcagct cctactacgc 60

ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaagaaccag 120

cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgacccc acaacaccaa 180

aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag gagcctgcac 240

ccacaaccac gaagagcgca ccacaacac caaaggagcc ggcccctacg actcctaagg 300

aaccctaaacc ggcaccaacc actccgga

328

<210> 17

<211> 108

<212> PRT

<213> Artificial

<220>

<223> 108 amino acids encoded by Lub:3 DNA insert (9 KEPAPTT sequences between S373 and E482 in SEQ ID NO: 15)

<400> 17

Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	Ser	Ala
1				5					10					15	

Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	Glu	Pro	Ala
			20					25					30		

Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	Glu	Pro	Ala
			35				40					45			

Pro	Thr	Thr	Thr	Lys	Ser	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro
	50					55					60				

Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	Glu	Pro	Ala	Pro
65				70						75				80	

Thr	Thr	Thr	Lys	Ser	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr
			85						90					95	

Thr	Pro	Lys	Glu	Pro	Lys	Pro	Ala	Pro	Thr	Thr	Pro
			100					105			

<210> 18

<211> 3210

<212> DNA

<213> Artificial

<220>

<223> recombinant PRG4-Lub:4 cDNA construct.

<400> 18

atggcatgga aaacacttcc catttacctg ttgttgctgc tgtctgtttt cgtgattcag	60
caagtttcat ctcaagattt atcaagctgt gcaggagat gtggggaagg gtattctaga	120
gatgccacct gcaactgtga ttataactgt caacactaca tggagtgtcg ccctgatttc	180
aagagagtct gcaactgcga gctttcctgt aaaggccgct gctttgagtc cttcgagaga	240
gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgtcg tcccgattat	300
gagagtttct gtgcagaagt gcataatccc acatcaccac catcttcaaa gaaagcacct	360
ccaccttcag gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca	420

aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt	480
tctgaaaatc aagagtcctc ctccagtagc agttcaagta gttcgtcgtc gacaatttgg	540
aaaatcaagt cttccaaaaa ttcagctgct aatagagaat tacagaagaa actcaaagta	600
aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgtagat	660
gaagctggaa gtggattgga caatggtgac ttcaaggta caactcctga cacgtctacc	720
acccaacaca ataaagtcag cacatctccc aagatcacia cagcaaaacc aataaatccc	780
agaccagtc ttccaccta ttctgatata tctaaagaga cgtctttgac agtgaataaa	840
gagacaacag ttgaaactaa agaaactact acaacaaata aacagacttc aactgatgga	900
aaagagaaga ctacttcgc taaagagaca caaagtatag agaaaacatc tgctaaagat	960
ttagcaccca catctaaagt gctggctaaa cctacaccca aagctgaaac tacaaccaa	1020
ggcctgctc tcaccactcc caaggagccc acgcccacca ctccaagga gcctgcatct	1080
accacaccca aagagcccac acctaccacc atcaagagcg cgccacaac tccaaaagag	1140
cccgaccta ccacgacaaa gtcagctcct actacgcca aagagccagc gccgacgact	1200
actaaagaac cggcacccac cagcctaaa gaaccagccc ctactacgac aaaggagcct	1260
gcaccacaaa ccacgaagag cgcaccaca acaccaaagg agccggcccc tacgactcct	1320
aaagaaccag ccctactac gacaaaggag cctgcaccca caaccacgaa gagcgacccc	1380
acaacaccaa aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag	1440
gagcctgcac ccacaaccac gaagagcgca ccacaacac caaaggagcc ggcccctacg	1500
actcctaagg aacccaaacc ggcaccaacc actccgaaa cacctcctcc aaccacttca	1560
gaggtctcta ctccaactac caccaaggag cctaccacta tccacaaaag ccctgatgaa	1620
tcaactcctg agctttctgc agaaccaca ccaaagctc ttgaaaacag tccaaggaa	1680
cctggtgtac ctacaactaa gacgccggcg gcgactaac ctgaaatgac tacaacagct	1740
aaagacaaga caacagaaag agacttacgt actacacctg aaactacaac tgctgcacct	1800
aagatgacaa aagagacagc aactacaaca gaaaaaacta cogaatccaa aataacagct	1860
acaaccacac aagtaacatc taccacaact caagatacca caccattcaa aattactact	1920
cttaaaacaa ctactcttgc acccaaagta actacaacaa aaaagacaat tactaccact	1980
gagattatga acaaacctga agaaacagct aaacccaaag acagagctac taattctaaa	2040
gcgacaactc ctaaacctca aaagccaacc aaagcaccca aaaaaccac ttctaccaa	2100
aagccaaaaa caatgcctag agtgagaaaa ccaagacga caccaactcc ccgcaagatg	2160
acatcaacaa tgccagaatt gaaccctacc tcaagaatag cagaagccat gctccaaacc	2220

accaccagac ctaaccaaac tccaaactcc aaactagttg aagtaaattcc aaagagtga 2280
 gatgcagggtg gtgctgaagg agaaacacct catatgcttc tcaggcccca tgtgttcatg 2340
 cctgaagtta ctcccgacat ggattactta ccgagagtac ccaatcaagg cattatcatc 2400
 aatcccatgc tttccgatga gaccaatata tgcaatggta agccagtaga tggactgact 2460
 actttgcgca atgggacatt agttgcattc cgagggtcatt atttctggat gctaagtcca 2520
 ttcagtccac catctccagc tcgcagaatt actgaagttt ggggtattcc ttccccatt 2580
 gatactgttt ttactaggtg caactgtgaa ggaaaaactt tcttctttaa ggattctcag 2640
 tactggcggtt ttaccaatga tataaaagat gcagggtacc ccaaaccaat tttcaaagga 2700
 tttggaggac taactggaca aatagtggca gcgctttcaa cagctaaata taagaactgg 2760
 cctgaatctg tgtatTTTTT caagagaggt ggcagcattc agcagtatat ttataaacag 2820
 gaacctgtac agaagtgcc tggaagaagg cctgctctaa attatccagt gtatggagaa 2880
 atgacacagg ttaggagacg tcgctttgaa cgtgctatag gacottctca aacacacacc 2940
 atcagaattc aatattcacc tgccagactg gcttatcaag acaaaggtgt ccttcataat 3000
 gaagttaaag tgagtatact gtggagagga cttccaaatg tggttacctc agctatatca 3060
 ctgccaaca tcagaaaacc tgacggctat gattactatg ctttttctaa agatcaatac 3120
 tataacattg atgtgcctag tagaacagca agagcaatta ctactcggtc tgggcagacc 3180
 ttatccaaag tctggtacaa ctgtccttaa 3210

<210> 19
 <211> 1069
 <212> PRT
 <213> Artificial

<220>
 <223> amino acid sequence of entire PRG4-LUB:4 protein.

<400> 19

Met	Ala	Trp	Lys	Thr	Leu	Pro	Ile	Tyr	Leu	Leu	Leu	Leu	Ser	Val	
1				5					10				15		
Phe	Val	Ile	Gln	Gln	Val	Ser	Ser	Gln	Asp	Leu	Ser	Ser	Cys	Ala	Gly
			20					25					30		
Arg	Cys	Gly	Glu	Gly	Tyr	Ser	Arg	Asp	Ala	Thr	Cys	Asn	Cys	Asp	Tyr
		35					40					45			
Asn	Cys	Gln	His	Tyr	Met	Glu	Cys	Cys	Pro	Asp	Phe	Lys	Arg	Val	Cys
	50					55					60				
Thr	Ala	Glu	Leu	Ser	Cys	Lys	Gly	Arg	Cys	Phe	Glu	Ser	Phe	Glu	Arg

65		70		75		80
Gly Arg Glu Cys Asp	Cys Asp Ala Gln Cys Lys Lys Tyr Asp	Lys Cys				
85		90			95	
Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser		100	105		110	
Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr		115	120		125	
Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys		130	135		140	
Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val		145	150		155	160
Ser Glu Asn Gln Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser		165		170		175
Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg		180		185		190
Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr		195	200		205	
Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser		210	215		220	
Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr		225	230		235	240
Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys		245		250		255
Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys		260		265		270
Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu		275	280		285	
Thr Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr		290	295		300	
Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp		305	310		315	320
Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu		325		330		335
Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro		340	345		350	
Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro		355	360		365	
Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr		370	375		380	

Thr	Thr	Lys	Ser	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	
385					390					395					400	
Thr	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	
			405						410					415		
Thr	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	Ser	Ala	Pro	Thr	Thr	Pro	
			420					425					430			
Lys	Glu	Pro	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Thr	
	435						440					445				
Lys	Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	Ser	Ala	Pro	Thr	Thr	Pro	Lys	
	450						455				460					
Glu	Pro	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	
465					470					475					480	
Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	Ser	Ala	Pro	Thr	Thr	Pro	Lys	Glu	
			485						490					495		
Pro	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Lys	Pro	Ala	Pro	Thr	Thr	Pro	
			500					505					510			
Glu	Thr	Pro	Pro	Pro	Thr	Thr	Ser	Glu	Val	Ser	Thr	Pro	Thr	Thr	Thr	
	515						520					525				
Lys	Glu	Pro	Thr	Thr	Ile	His	Lys	Ser	Pro	Asp	Glu	Ser	Thr	Pro	Glu	
	530					535					540					
Leu	Ser	Ala	Glu	Pro	Thr	Pro	Lys	Ala	Leu	Glu	Asn	Ser	Pro	Lys	Glu	
545					550					555					560	
Pro	Gly	Val	Pro	Thr	Thr	Lys	Thr	Pro	Ala	Ala	Thr	Lys	Pro	Glu	Met	
			565						570					575		
Thr	Thr	Thr	Ala	Lys	Asp	Lys	Thr	Thr	Glu	Arg	Asp	Leu	Arg	Thr	Thr	
			580					585					590			
Pro	Glu	Thr	Thr	Thr	Ala	Ala	Pro	Lys	Met	Thr	Lys	Glu	Thr	Ala	Thr	
	595						600					605				
Thr	Thr	Glu	Lys	Thr	Thr	Glu	Ser	Lys	Ile	Thr	Ala	Thr	Thr	Thr	Gln	
	610					615					620					
Val	Thr	Ser	Thr	Thr	Thr	Gln	Asp	Thr	Thr	Pro	Phe	Lys	Ile	Thr	Thr	
625					630					635					640	
Leu	Lys	Thr	Thr	Thr	Leu	Ala	Pro	Lys	Val	Thr	Thr	Thr	Lys	Lys	Thr	
			645						650					655		
Ile	Thr	Thr	Thr	Glu	Ile	Met	Asn	Lys	Pro	Glu	Glu	Thr	Ala	Lys	Pro	
			660					665					670			
Lys	Asp	Arg	Ala	Thr	Asn	Ser	Lys	Ala	Thr	Thr	Pro	Lys	Pro	Gln	Lys	
	675						680					685				
Pro	Thr	Lys	Ala	Pro	Lys	Lys	Pro	Thr	Ser	Thr	Lys	Lys	Pro	Lys	Thr	
	690					695					700					

Met Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg Lys Met
 705 710 715 720
 Thr Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala Glu Ala
 725 730 735
 Met Leu Gln Thr Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser Lys Leu
 740 745 750
 Val Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu Gly Glu
 755 760 765
 Thr Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu Val Thr
 770 775 780
 Pro Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile Ile Ile
 785 790 795 800
 Asn Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro Val
 805 810 815
 Asp Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe Arg Gly
 820 825 830
 His Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro Ala Arg
 835 840 845
 Arg Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr Val Phe
 850 855 860
 Thr Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp Ser Gln
 865 870 875 880
 Tyr Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro Lys Pro
 885 890 895
 Ile Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala Ala Leu
 900 905 910
 Ser Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe Phe Lys
 915 920 925
 Arg Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro Val Gln
 930 935 940
 Lys Cys Pro Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr Gly Glu
 945 950 955 960
 Met Thr Gln Val Arg Arg Arg Arg Phe Glu Arg Ala Ile Gly Pro Ser
 965 970 975
 Gln Thr His Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu Ala Tyr
 980 985 990
 Gln Asp Lys Gly Val Leu His Asn Glu Val Lys Val Ser Ile Leu Trp
 995 1000 1005
 Arg Gly Leu Pro Asn Val Val Thr Ser Ala Ile Ser Leu Pro Asn

1010	1015	1020
Ile Arg Lys Pro Asp Gly Tyr Asp Tyr Tyr Ala Phe Ser Lys Asp		
1025	1030	1035
Gln Tyr Tyr Asn Ile Asp Val Pro Ser Arg Thr Ala Arg Ala Ile		
1040	1045	1050
Thr Thr Arg Ser Gly Gln Thr Leu Ser Lys Val Trp Tyr Asn Cys		
1055	1060	1065

Pro

<210> 20
 <211> 421
 <212> DNA
 <213> Artificial

<220>

<223> Lub:4 DNA insert from cDNA cassette-1 and three synthetic cDNA cassette-2 sequences.

<400> 20
 gcgcgcccac aactccaaaa gagcccgac ctaccacgac aaagtcagct cctactacgc 60
 ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaagaaccag 120
 cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgacccc acaacaccaa 180
 aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag gagcctgcac 240
 ccacaaccac gaagagcgca ccacaacac caaaggagcc ggcccctacg actcctaaag 300
 aaccagcccc tactacgaca aaggagcctg caccacaac cacgaagagc gcaccacaaa 360
 caccaaagga gccggcccct acgactccta aggaacccaa accggcacca accactccgg 420
 a 421

<210> 21
 <211> 139
 <212> PRT
 <213> Artificial

<220>

<223> 139 amino acids encoded by Lub:4 DNA insert (12 KEPAPTT sequences between S373 and E513 in SEQ ID NO: 19)

<400> 21

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
1 5 10 15
Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
20 25 30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
 35 40 45

Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro
 50 55 60

Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro
 65 70 75 80

Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
 85 90 95

Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr
 100 105 110

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
 115 120 125

Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
 130 135

<210> 22

<211> 3303

<212> DNA

<213> Artificial

<220>

<223> Recombinant PRG4-Lub:5 cDNA construct

<400> 22

atggcatgga aaacacttcc catttacctg ttgttgetgc tgtctgtttt cgtgattcag 60

caagtttcat ctcaagattt atcaagctgt gcagggagat gtggggaagg gtattctaga 120

gatgccacct gcaactgtga ttataactgt caacactaca tggagtgtcg ccctgatttc 180

aagagagtct gcaactgcga gctttcctgt aaaggccgct gctttgagtc cttcgagaga 240

gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgtcg tcccgattat 300

gagagtttct gtgcagaagt gcataatccc acatcaccac catcttcaaa gaaagcacct 360

ccaccttcag gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca 420

aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt 480

tctgaaaatc aagagtcctc ctccagtagc agttcaagta gttcgtcgtc gacaatttgg 540

aaaatcaagt cttccaaaaa ttcagctgct aatagagaat tacagaagaa actcaaagta 600

aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgtagat 660

gaagctggaa gtggattgga caatggtgac ttcaaggtca caactcctga cacgtctacc 720

acccaacaca ataaagtcag cacatctccc aagatcacia cagcaaaacc aataaatccc 780

agaccagtc ttccacctaa ttctgatata tctaaagaga cgtctttgac agtgaataaa 840

gagacaacag	ttgaaactaa	agaaactact	acaacaaata	aacagacttc	aactgatgga	900
aaagagaaga	ctacttccgc	taaagagaca	caaagtatag	agaaaacatc	tgctaaagat	960
ttagcaccga	catctaaagt	gctggctaaa	cctacaccga	aagctgaaac	tacaacaaaa	1020
ggccctgctc	tcaccactcc	caaggagccc	acgcccacca	ctcccaagga	gcctgcatct	1080
accacaccga	aagagcccac	acctaccacc	atcaagagcg	cgcccacaac	tccaaaagag	1140
cccgcacctc	ccacgacaaa	gtcagctcct	actacgcccga	aagagccagc	gccgacgact	1200
actaaagaac	cggcaccac	cacgcctaaa	gaaccagccc	ctactacgac	aaaggagcct	1260
gcaccacaaa	ccacgaagag	cgcaccacga	acaccaaagg	agccggcccc	tacgactcct	1320
aaagaaccag	cccctactac	gacaaaggag	cctgcaccga	caaccacgaa	gagcgcaccc	1380
acaacaccaa	aggagccggc	ccctacgact	cctaaagaac	cagcccctac	tacgacaaaag	1440
gagcctgcac	ccacaaccac	gaagagcgca	cccacaacac	caaaggagcc	ggcccctacg	1500
actcctaaag	aaccagcccc	tactacgaca	aaggagcctg	caccacaaac	cacgaagagc	1560
gcaccacaaa	caccaaagga	gccggccccct	acgactccta	aggaacccaa	accggcacca	1620
accactccgg	aaacacctcc	tccaaccact	tcagaggtct	ctactccaac	taccaccaag	1680
gagcctacca	ctatccacaa	aagccctgat	gaatcaactc	ctgagctttc	tgcagaaccc	1740
acacaaaaag	ctcttgaaaa	cagtcccaag	gaacctggtg	tacctacaac	taagacgccg	1800
gcggcgacta	aacctgaaat	gactacaaca	gctaaagaca	agacaacaga	aagagactta	1860
cgtactacac	ctgaaactac	aactgctgca	cctaagatga	caaaagagac	agcaactaca	1920
acagaaaaaa	ctaccgaatc	caaaataaca	gctacaacca	cacaagtaac	atctaccaca	1980
actcaagata	ccacaccatt	caaaattact	actcttaaaa	caactactct	tgaccccaaa	2040
gtaactacaa	caaaaaagac	aattactacc	actgagatta	tgaacaaacc	tgaagaaaca	2100
gctaaaccaa	aagacagagc	tactaattct	aaagcgacaa	ctcctaaacc	tcaaaagcca	2160
accaaagcac	caaaaaaacc	cacttctacc	aaaaagccaa	aaacaatgcc	tagagtgaga	2220
aaaccaaaga	cgacaccaac	tccccgcaag	atgacatcaa	caatgccaga	attgaaccct	2280
acctcaagaa	tagcagaagc	catgctccaa	accaccacca	gacctaacca	aactccaaac	2340
tccaaactag	ttgaagtaaa	tccaaagagt	gaagatgcag	gtggtgctga	aggagaaaca	2400
cctcatatgc	ttctcaggcc	ccatgtgttc	atgcctgaag	ttactcccga	catggattac	2460
ttaccgagag	tacccaatca	aggcattatc	atcaatccca	tgctttccga	tgagaccaat	2520
atatgcaatg	gtaagccagt	agatggactg	actactttgc	gcaatgggac	attagttgca	2580
ttccgaggtc	attattttctg	gatgctaagt	ccattcagtc	caccatctcc	agctcgcaga	2640

```

attactgaag tttggggtat tccttcccc attgatactg tttttactag gtgcaactgt 2700
gaaggaaaaa ctttcttctt taaggattct cagtactggc gttttaccaa tgatataaaa 2760
gatgcagggt accccaaacc aattttcaaa ggatttggag gactaactgg acaaatagtg 2820
gcagcgcttt caacagctaa atataagaac tggcctgaat ctgtgtattt tttcaagaga 2880
ggtggcagca ttcagcagta tattttataaa caggaacctg tacagaagtg ccctggaaga 2940
aggcctgctc taaattatcc agtgtatgga gaaatgacac aggttaggag acgtcgcttt 3000
gaacgtgcta taggaccttc tcaaacacac accatcagaa ttcaatatcc acctgccaga 3060
ctggcttate aagacaaagg tgtccttcat aatgaagta aagtgagtat actgtggaga 3120
ggacttccaa atgtggttac ctacagctata tcaactgccca acatcagaaa acctgacggc 3180
tatgattact atgccttttc taaagatcaa tactataaca ttgatgtgcc tagtagaaca 3240
gcaagagcaa ttactactcg ttctgggcag accttatcca aagtctggta caactgtcct 3300
taa 3303

```

<210> 23
 <211> 1100
 <212> PRT
 <213> Artificial

<220>
 <223> Amino acid sequence of entire PRG4-LUB:5 protein.

<400> 23

```

Met Ala Trp Lys Thr Leu Pro Ile Tyr Leu Leu Leu Leu Leu Ser Val
1          5          10          15
Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly
20          25          30
Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr
35          40          45
Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys
50          55          60
Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg
65          70          75          80
Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys
85          90          95
Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser
100         105         110
Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr
115         120         125

```

Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys
 130 135 140
 Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val
 145 150 155 160
 Ser Glu Asn Gln Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
 165 170 175
 Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg
 180 185 190
 Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr
 195 200 205
 Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser
 210 215 220
 Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr
 225 230 235 240
 Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys
 245 250 255
 Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys
 260 265 270
 Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu
 275 280 285
 Thr Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr
 290 295 300
 Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp
 305 310 315 320
 Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu
 325 330 335
 Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro
 340 345 350
 Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro
 355 360 365
 Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
 370 375 380
 Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
 385 390 395 400
 Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
 405 410 415
 Thr Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro
 420 425 430
 Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr

435		440		445
Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys				
450		455		460
Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys				
465		470		475
Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu				
		485		490
				495
Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu				
		500		505
				510
Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro				
		515		520
				525
Ala Pro Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro Glu				
		530		535
				540
Thr Pro Pro Pro Thr Thr Ser Glu Val Ser Thr Pro Thr Thr Thr Lys				
		545		550
				555
Glu Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr Pro Glu Leu				
		565		570
				575
Ser Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro Lys Glu Pro				
		580		585
				590
Gly Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro Glu Met Thr				
		595		600
				605
Thr Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg Thr Thr Pro				
		610		615
				620
Glu Thr Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr Ala Thr Thr				
		625		630
				635
Thr Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr Thr Gln Val				
		645		650
				655
Thr Ser Thr Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile Thr Thr Leu				
		660		665
				670
Lys Thr Thr Thr Leu Ala Pro Lys Val Thr Thr Thr Lys Lys Thr Ile				
		675		680
				685
Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala Lys Pro Lys				
		690		695
				700
Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro Gln Lys Pro				
		705		710
				715
Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro Lys Thr Met				
		725		730
				735
Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg Lys Met Thr				
		740		745
				750

Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala Glu Ala Met
 755 760 765
 Leu Gln Thr Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser Lys Leu Val
 770 775 780
 Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu Gly Glu Thr
 785 790 795 800
 Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu Val Thr Pro
 805 810 815
 Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile Ile Ile Asn
 820 825 830
 Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro Val Asp
 835 840 845
 Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe Arg Gly His
 850 855 860
 Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro Ala Arg Arg
 865 870 875 880
 Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr Val Phe Thr
 885 890 895
 Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp Ser Gln Tyr
 900 905 910
 Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro Lys Pro Ile
 915 920 925
 Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala Ala Leu Ser
 930 935 940
 Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe Phe Lys Arg
 945 950 955 960
 Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro Val Gln Lys
 965 970 975
 Cys Pro Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr Gly Glu Met
 980 985 990
 Thr Gln Val Arg Arg Arg Arg Phe Glu Arg Ala Ile Gly Pro Ser Gln
 995 1000 1005
 Thr His Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu Ala Tyr
 1010 1015 1020
 Gln Asp Lys Gly Val Leu His Asn Glu Val Lys Val Ser Ile Leu
 1025 1030 1035
 Trp Arg Gly Leu Pro Asn Val Val Thr Ser Ala Ile Ser Leu Pro
 1040 1045 1050
 Asn Ile Arg Lys Pro Asp Gly Tyr Asp Tyr Tyr Ala Phe Ser Lys
 1055 1060 1065

Asp Gln Tyr Tyr Asn Ile Asp Val Pro Ser Arg Thr Ala Arg Ala
 1070 1075 1080

Ile Thr Thr Arg Ser Gly Gln Thr Leu Ser Lys Val Trp Tyr Asn
 1085 1090 1095

Cys Pro
 1100

<210> 24
 <211> 514
 <212> DNA
 <213> Artificial

<220>
 <223> Lub:5 DNA insert from cDNA cassette-1 and four synthetic cDNA
 cassette-2 sequences

<400> 24
 gcgcgcccac aactccaaaa gagcccgac ctaccacgac aaagtcagct cctactacgc 60
 ccaagagacc agcgccgacg actactaaag aaccggcacc caccacgcct aaagaaccag 120
 cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgacccc acaacaccaa 180
 aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag gagcctgcac 240
 ccacaaccac gaagagcgca ccacaacac caaaggagcc ggcccctacg actcctaaag 300
 aaccagcccc tactacgaca aaggagcctg caccacaaac cacgaagagc gcacccacaa 360
 caccaaagga gccggcccct acgactccta aagaaccagc ccctactacg acaaaggagc 420
 ctgcacccac aaccacgaag agcgcaacca caacaccaaa ggagccggcc cctacgactc 480
 ctaaggaacc caaaccggca ccaaccactc cgga 514

<210> 25
 <211> 170
 <212> PRT
 <213> Artificial

<220>
 <223> 170 amino acids encoded by Lub:5 DNA insert (15 KEPAPTT sequences
 between S373 and E544 in SEQ ID NO: 23)

<400> 25

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
 1 5 10 15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
 20 25 30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
 35 40 45

Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro
50 55 60

Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro
65 70 75 80

Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
85 90 95

Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr
100 105 110

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
115 120 125

Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr Thr
130 135 140

Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Pro
145 150 155 160

Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
165 170

<210> 26

<211> 45

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence "APTTTPKEPAPTTTTSAPTTPKEPAPTTT
KEPAPTTTPKEPAPTTTK" (45 amino acids) in preferred PRG4-LUB:N
protein

<400> 26

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
1 5 10 15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
20 25 30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys
35 40 45

<210> 27

<211> 31

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence "KEPAPTTTKEPAPTTTTSAPTTPKEPAPTTTP" (31 amino
acids) repeated N-1 times in preferred PRG4-LUB:N protein

<400> 27

40

Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr Thr Thr
1 5 10 15

Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Pro
20 25 30

<210> 28

<211> 22

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence "EPAPTTTKSAPTTTPKEPAPTTTP" (22 amino acids)
joining SEQ ID NO: 26 to (N-2) repeats of SEQ ID NO: 27 in
preferred PRG4-LUB:N protein where N = 3 or more.

<400> 28

Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu
1 5 10 15

Pro Ala Pro Thr Thr Pro
20

<210> 29

<211> 10

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence "KEPKPAPTTTP" (10 amino acids) in preferred
PRG4-LUB:N protein where N = 2 or more.

<400> 29

Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
1 5 10